Abstract

The present invention is directed to a method for identification of a Gram positive pathogenic bacterium comprising an amplification step with at least a first set of amplification primers capable of amplifying a preselected nucleic acid sequence region from a first predetermined sub-group of pathogenic Gram positive bacteria, and a detection step with at least a first hybridization reagent capable of specifically detecting a preselected nucleic acid sequence region from the first predetermined sub-group of pathogenic Gram positive bacteria, said detection step comprising steps monitoring whether hybridization has occurred at a preselected temperature, said occurrence of hybridization being indicative for at least the genus of a pathogenic organism present in the sample, and monitoring temperature dependence of hybridization, said temperature dependence being indicative for at least the species of the pathogenic Gram positive bacterium.